

Figure 1A

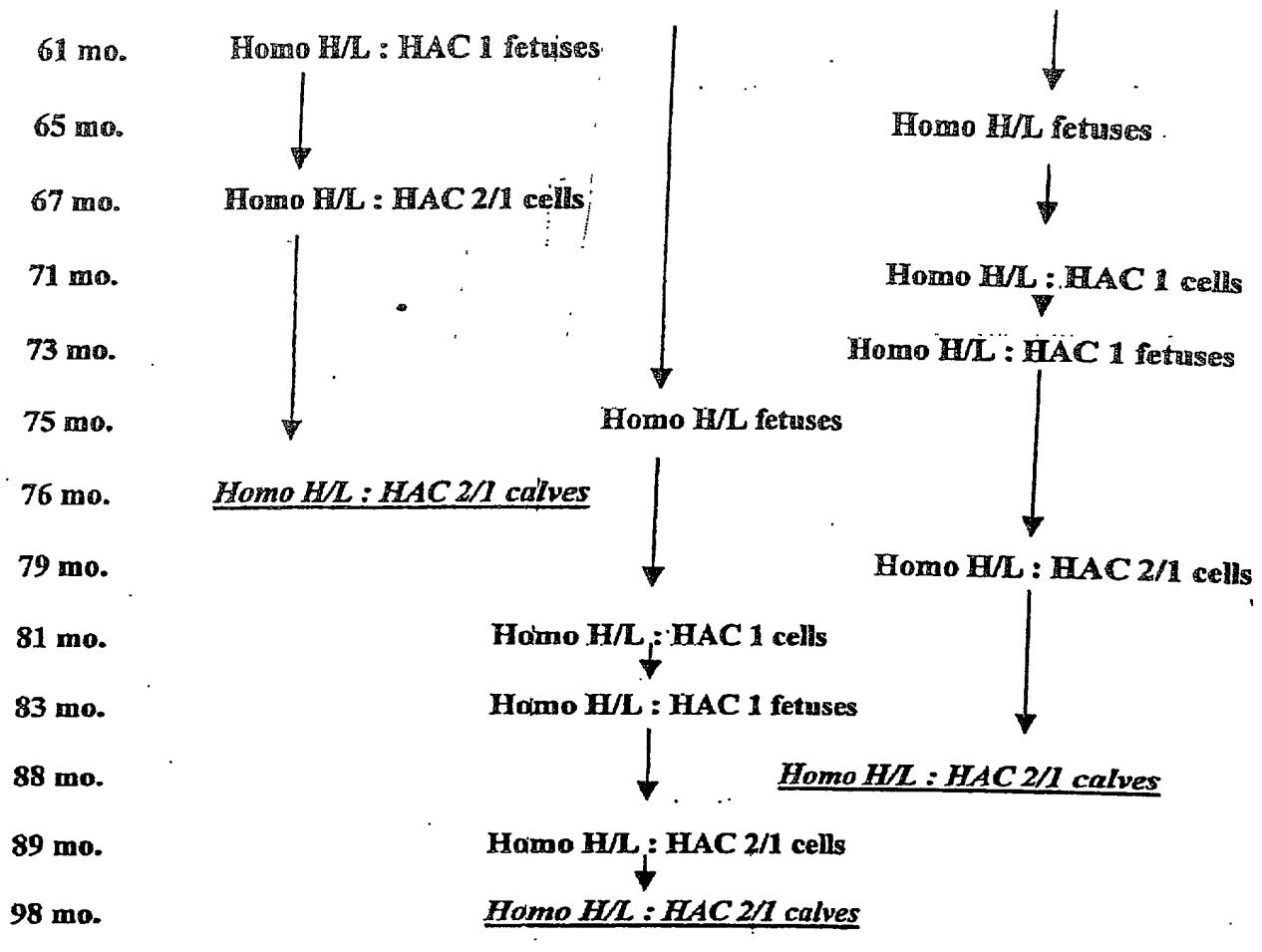


Figure 1A continued

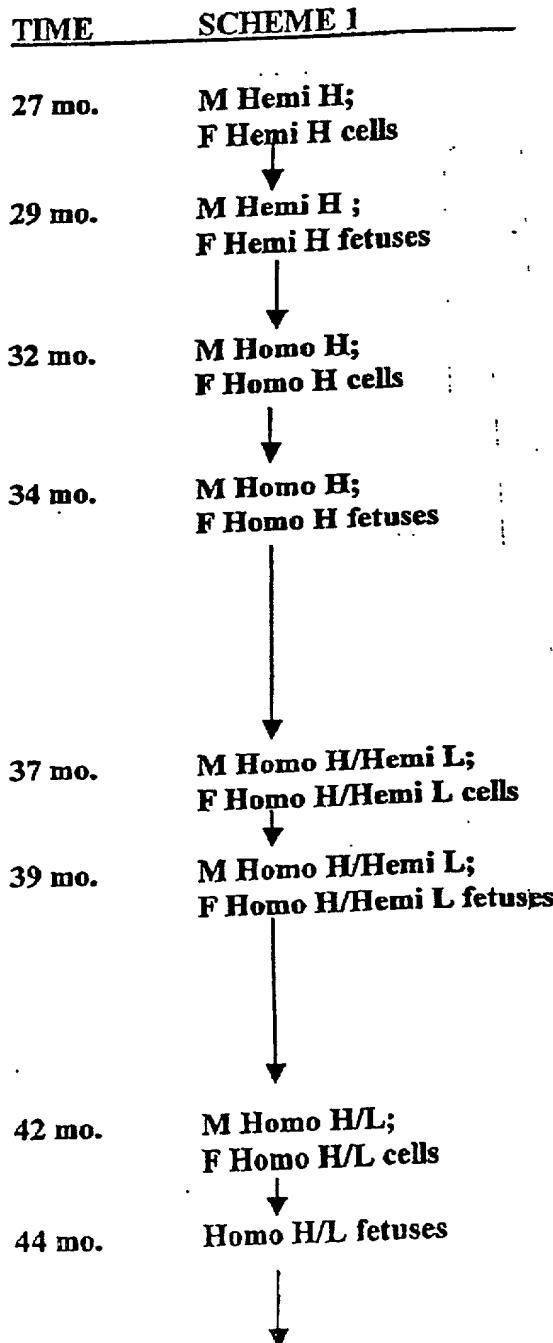


Figure 1B

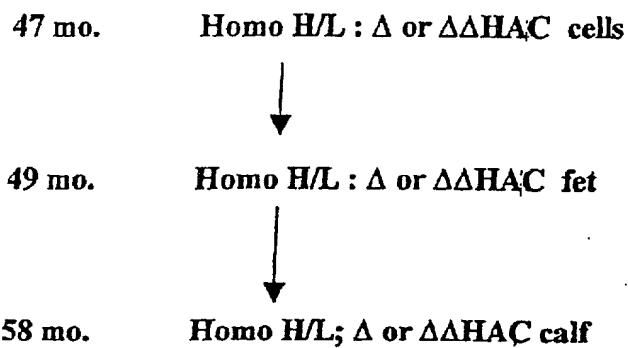


Figure 1B continued

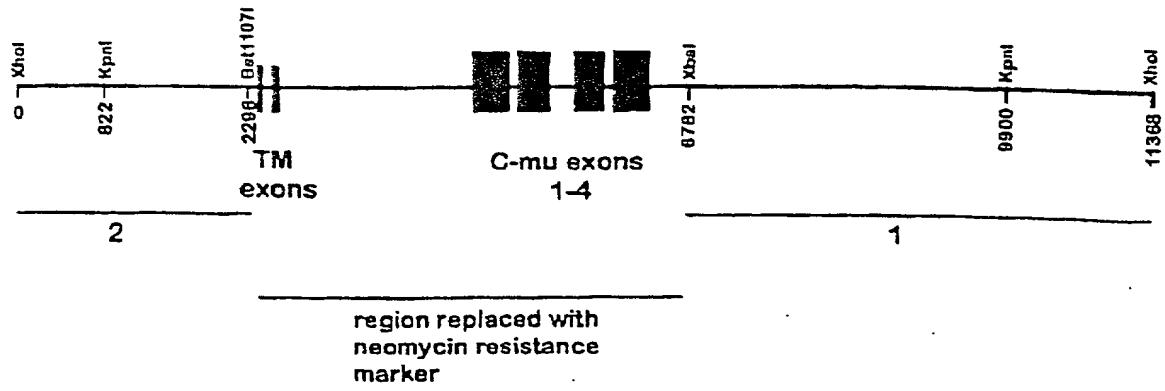


Figure 2A

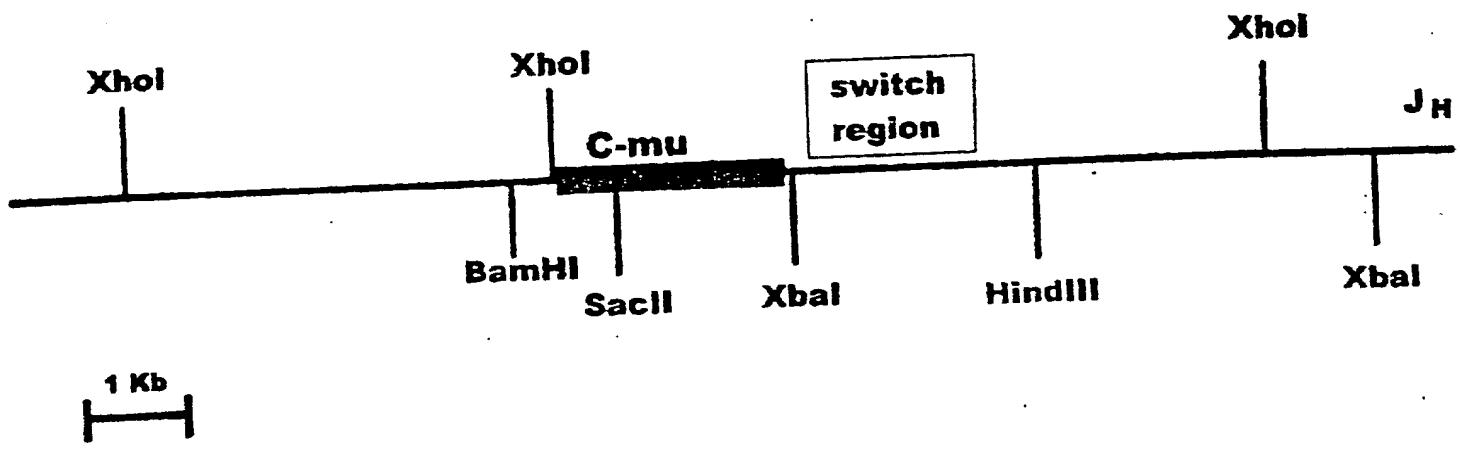
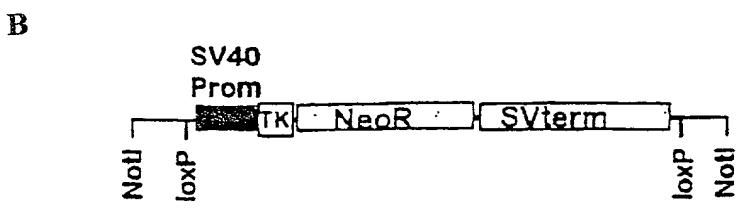
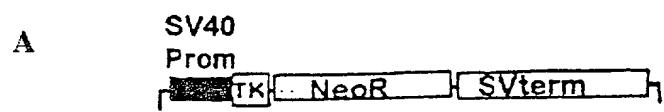


Figure 2B



Figures 3A and 3B

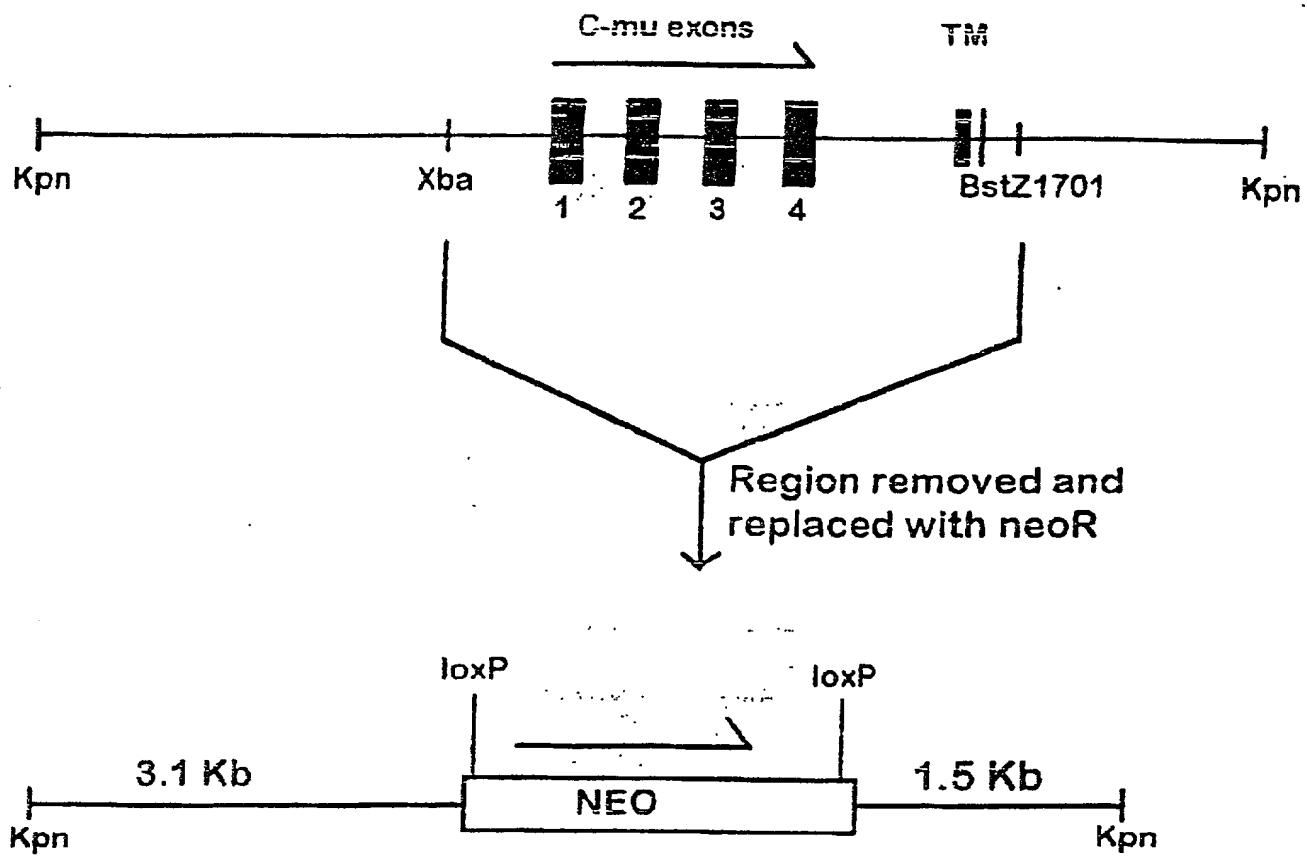


Figure 3C

SEQ ID NO: 47

ggtaccgaaaggcgccctgaacattctgcagtgagggagccgcactgagaaagctgcattcatgcgcgggagggagccagc
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agcgtacgaatgcattgataaaaatgcacccctgagacaataattcttaaacatgcacttgaaaatgaatataagtgagcagtgtat
aggctctgaatgaaataccctccaaacaggctgctgagaaccggccaggagcaggaaacggactccccgtggagcccccaagg
agccagccctgatgataccctggccctggccctcctcagcgtggagagagccagctccctgtttcatgcctggccctgtgg
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aggcaccctgcctgcccggagccctcaccaacgttccccccgcctgatgggtggccgaaaaggacaccgttaaccaga
actgcctccaggagcctactgtggaggccgttctctggaccaggccactccactccctggatagtcactgtcaggcc
cctggggcccccacaagaggcgtcctggaaagccccagtcctccagccctgaaattgcctccctggagagccagatcac
cctcaccagctccctccctgcctccccccagggtctccatcccacccgccttaccctggcgttgcgtcacagctaa
cctgacccctgggttcgagcgtgccgccttcagggcttccctccgtgcctccagtcctgcaccctccctgc
cctgagacttccttcaccccccaggccgttctggcctgcagggtctcgcgtccctcagggcacatgtggctgca
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gggaatggcggcagagagagggcggggtgtcctgggtggcagggtctcatggatgcacacagccggccggc
aggccacctggaaaccagtctggatctgcaactcgccatgttctgcattggaccagcccaagacaccaccccg
gtggcgccactggccctgggaggagacacatgtccctcccatcagcaatgggtcagcactaggatatgc
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Figure 3D

SEQ ID NO: 48

Figure 3E

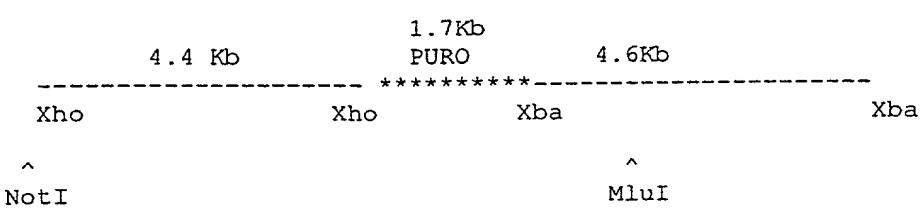


Figure 3F

SEQ ID NO: 60

1 atgagattcc ctgctcagct cctggggctc ctcctgtctt gggtcccagg
51 atccagtggg gatgttgtgc tgaccacagac tccccctctcc ctgtcttatca
101 tccctggaga gacggtctcc atctcctgca agtctactca gagtctgaaa
151 tatagtatg gaaaaaccta tttgtactgg cttcaacata aaccaggcca
201 atcaccacag ctttgatct atgctgtttc cagccgttac actggggtcc
251 cagacagggtt cactggcagt gggtcagaaa cagattcac acttacgatc
301 aacagtgtgc aggctgagga tgttgagtc tattactgtc ttcaaacaac
351 atatgtccca aatactttcg gccaaaggaaac caaggttagag atcaaaaggt
401 ctgatgctga gccatccgtc ttcctcttca aaccatctga tgagcagctg
451 aagaccggaa ctgtctctgt cgtgtgcttg gtgaatgatt tctaccccaa
501 agatatcaat gtcaagtgg aagtggatgg ggtaactcag agcagcagca
551 acttccaaaa cagtttcaca gaccaggaca gcaagaaaag cacctacagc
601 ctcagcagca tcctgacact gcccagctca gagtaccaaa gccatgacgc
651 ctatacgtgt gaggtcagcc acaagagcct gactaccacc ctcgtcaaga
701 gcttcagtaa gaacgagtgt tag

#22 fragments

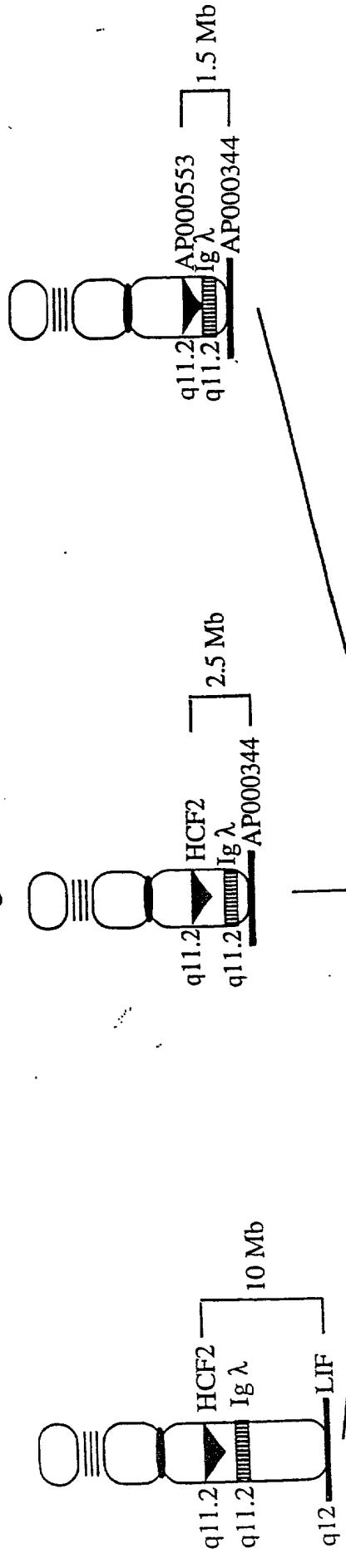
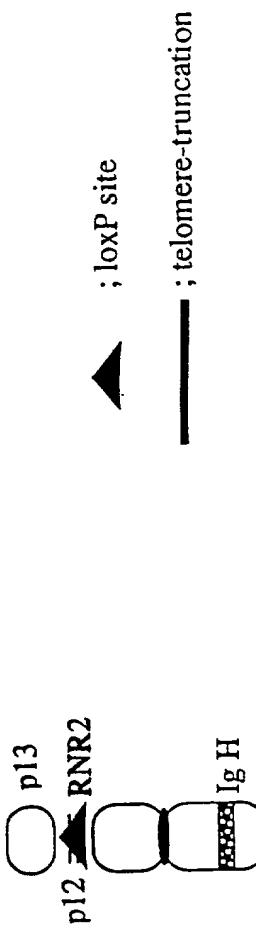
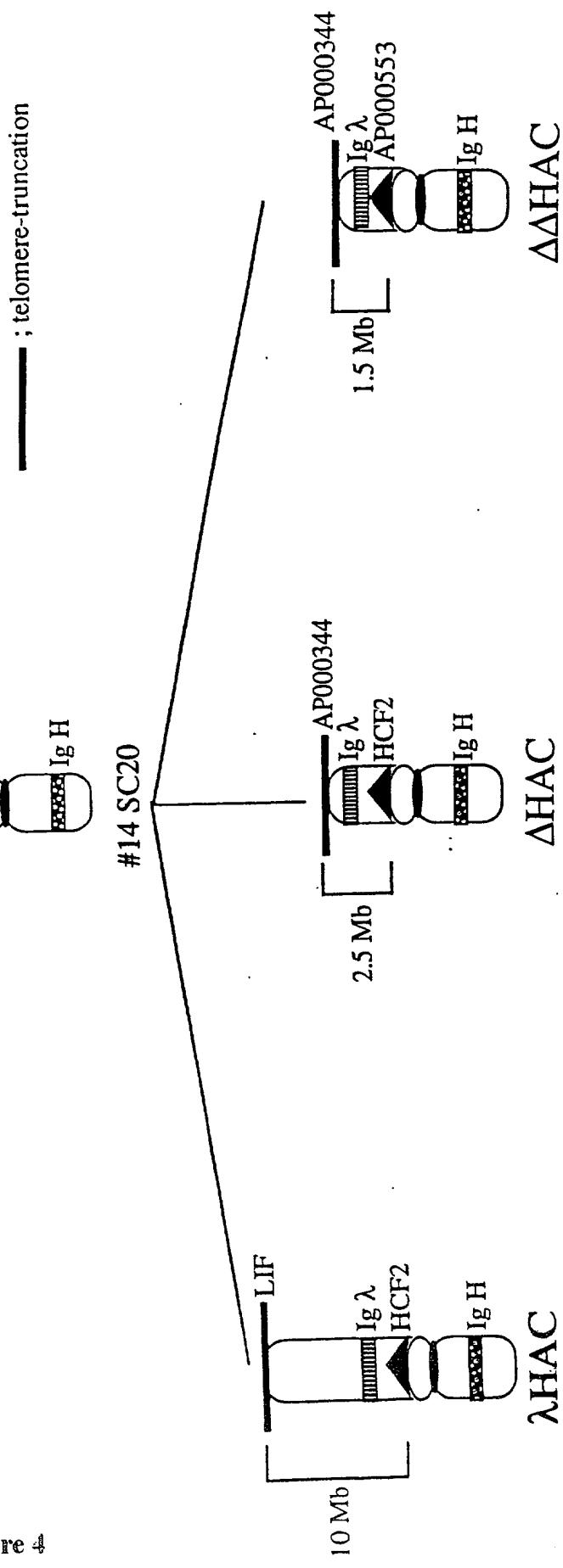


Figure 4



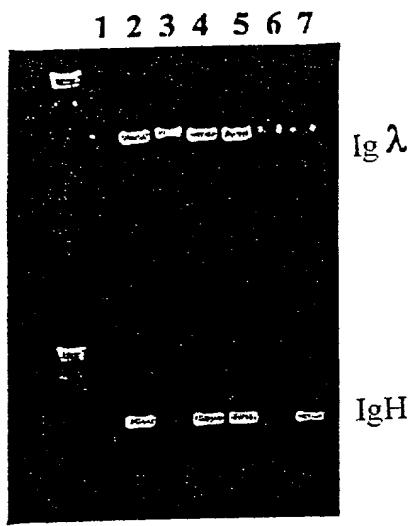
#14 SC20



Δ HAC

λ HAC

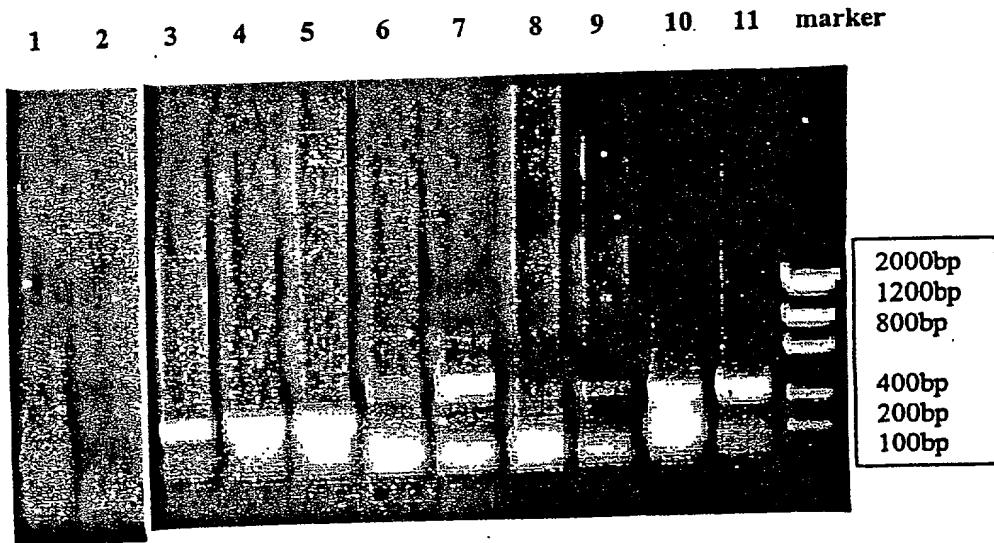
▲ ; loxP site
— ; telomere-truncation



1. Bovine genomic DNA (negative control)
2. Fetus 5968 genomic DNA at 56 days
3. Fetus 5983 genomic DNA at 56 days
4. Fetus 6032 genomic DNA at 58 days
5. Fetus 6045 genomic DNA at 56 days
6. Fetus 5846 genomic DNA at 79 days
7. Fetus 5996 genomic DNA at 77 days

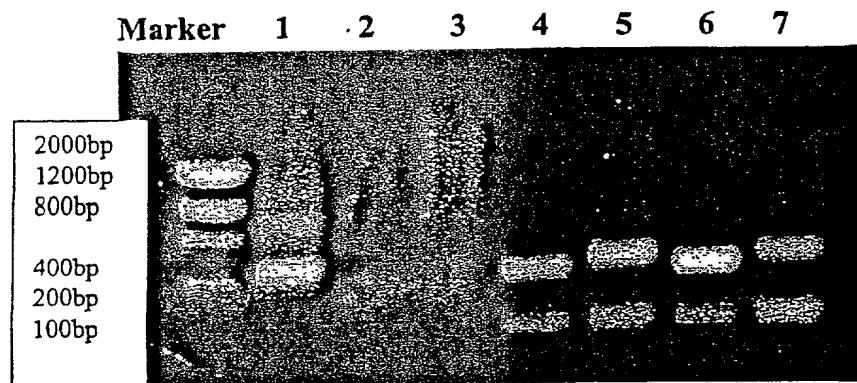
<u>Fetus</u>	<u>Clone</u>	<u>IgH</u>	<u>Ig λ</u>
5968	B4-2	Pos	Pos
5983	B2-13	Neg	Neg
6032	B4-8	Pos	Pos
6045	B2-22	Pos	Pos
5846	B4-8	Neg	Neg
5996	B4-2	Pos	Neg

Figure 5



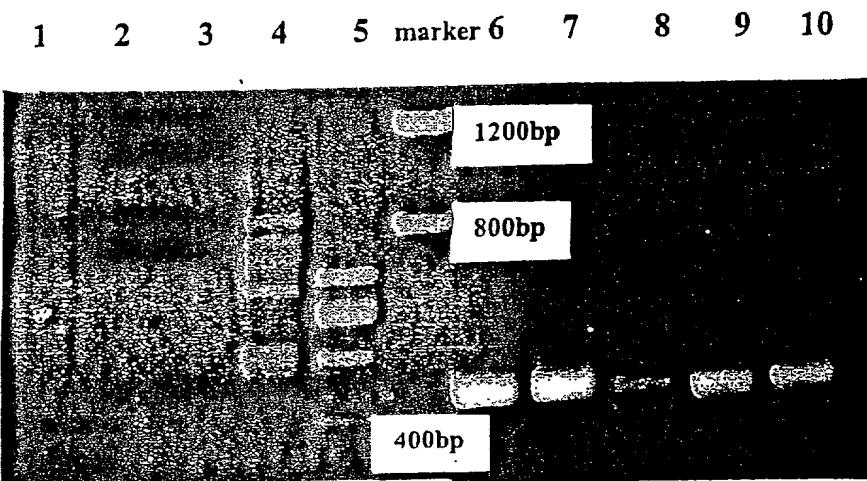
1. Human mu constant region in bovine liver cDNA from fetus 5996.
2. Human mu constant region in bovine brain cDNA from fetus 5996.
3. Human mu constant region in bovine spleen cDNA from fetus 5996.
4. Human mu constant region in human spleen cDNA.
5. Human mu constant region in mouse spleen CDNA with HAC.
6. Bovine rearranged Cmu heavy chain in bovine spleen cDNA from fetus 5996.
7. Bovine rearranged Cmu heavy chain in human spleen cDNA.
8. Bovine rearranged Cmu heavy chain in mouse spleen CDNA with HAC.
9. GAPDH primers in bovine spleen cDNA from fetus 5996.
10. GAPDH primers in bovine liver cDNA
11. GAPDH primers in mouse spleen CDNA with HAC.

Figure 6



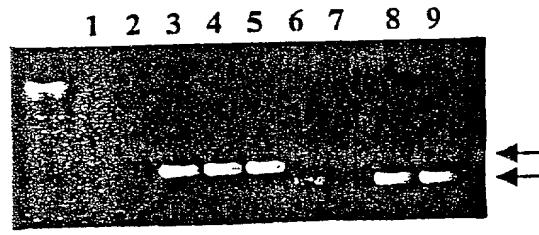
1. GAPDH primers in bovine liver cDNA
2. Bovine rearranged Cmu heavy chain in bovine brain cDNA from fetus 5996.
3. Bovine rearranged Cmu heavy chain in bovine liver cDNA from fetus 5996.
4. GAPDH primers in bovine spleen cDNA from fetus 5996.
5. Bovine rearranged Cmu heavy chain in bovine spleen cDNA from fetus 5996.
6. GAPDH primers in bovine brain cDNA from fetus 5996.
7. Bovine rearranged Cmu heavy chain positive control.

Figure 7



1. Human rearranged Cmu heavy chain in mouse spleen cDNA with HAC (+ control).
2. Human rearranged Cmu heavy chain in bovine liver cDNA from fetus.
3. Human rearranged Cmu heavy chain in bovine brain cDNA from fetus 5996
4. Human rearranged Cmu heavy chain in human spleen cDNA (+ control).
5. Human rearranged Cmu heavy chain in bovine spleen cDNA from fetus 5996.
6. GAPDH primers in bovine spleen cDNA from fetus 5996.
7. GAPDH primers in mouse spleen cDNA with HAC
8. GAPDH primers in bovine brain cDNA from fetus 5996.
9. GAPDH primers in bovine liver cDNA from fetus 5996.
10. GAPDH primers positive control.

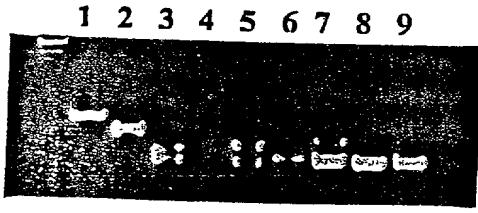
Figure 8



1. Mouse spleen (negative control)
2. Bovine spleen (negative control)
3. Fetus 5996 brain
4. Fetus 5996 liver
5. Fetus 5996 liver
6. Fetus 5996 spleen
7. Fetus 5996 spleen
8. Δ HAC-chimeric mouse spleen
(positive control)
9. Human spleen (positive control)

↔ Unspliced genomic fragment
Spliced transcript

Figure 9



1. Mouse spleen (negative control)
2. Bovine spleen (negative control)
3. Fetus 5996 brain
4. Fetus 5996 liver
5. Fetus 5996 liver
6. Fetus 5996 spleen
7. Fetus 5996 spleen
8. Δ HAC-chimeric mouse spleen
(positive control)
9. Human spleen (positive control)

Figure 10

Figure 11A SEQ ID NO: 49

5'
GGGAAGGAAGTCCTGTGCGACCANCCAACGGCCACGCTGCTCGTATCCGACG
GGGAATTCTCACAGGAGACGAGGGGGAAAAGGGTTGGGGCGGATGCAGTCC
CTGAGGAGACGGTGACCAAGGGTCCNTGGCCSAGNNNGICAA3'

Figure 11B SEQ ID NOs: 50 and 51

V-D-J region | →constant mu region

Subject: 5'
tttgactactggggccagggAACCCtggtcaccgtctcctcaggagtgcatccgccccca
-----nn-----n-----

Query

Subject:
accctttccccctcgtcctctgtgagaattccccgtcgatcgcgcgtggccgtt

Query

Subject: 5'
ggctgcctcgacaggacttcctcccgaactccatcactttcccg 3'
---n---g----- Cmul primer
~

SEQ ID NO₃ 52 and 53

10 19 28 37 46 55
5' GGA GGC TTG GTC AAG CCT GGA GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA
G G L V K P G G S L R L S C A A S G

64 73 82 91 100 109
TTC ACC TTC ACT GAC TAC TAC ATG AGC TGG ATC CGC CAG GCT CCA GGG AAG GGG
F T F S D Y Y M S W I R Q A P G K G

118 127 136 145 154 163
CTG GAG TGG GTT TCA TAC ATT AGT AGT GGT AGT ACC ATA TAC TAC GCA GAC
L E W V S Y I S S S G S T I Y Y A D
VH3-11

172 181 190 199 208 217
TCT GTG AAG GGC CGA TTC ACC ATC TCC AGG GAC AAC GCC AAG AAC TCA CTG TAT
S V K G R F T I S R D N A K N S L Y

226 235 244 253 262 271
CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC ACG GCT GTG TAT TAC TGT GCG AGA
L Q M N S L R A E D T A V Y Y C A R

280 289 298 307 316 325
ATA ACT GGG GAT GCT TTT GAT ATC TGG GGC CAA GGG ACA ATG GTC ACC GTC TCT
I T G D A F D I W G Q G T M V T V S
D7-27 JH3

334 343 352 361 370 379
TCA GGG AGT GCA TCC GCC CCA ACC CTT TTC CCC CTC GTC TCC TGT GAG AAT TCC
S G S A S A P T L F P L V S C E N S

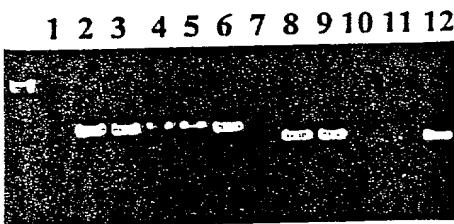
388 C4
CCG TCG GAT AGC AGC 3'
P S D T S

Figure 12A

SEQ ID NOS: 54 and 55

GTG GAG TCT GGG GGA GGC TTG GTA CAG CCT GGG AGG TCC CTG AGA CTC TCC TGT
V E S G G L V Q P G R S L R L S C
GCA GCG TCA GGA TTC ACC TTC AGG AAC TTT GGC ATG CAC TGG GTC CGC CAG GCT
A A S G F T F R N F G M H W V R Q A
VH3-33
CCA GGC AAG GGG CTG GAG TGG GTG ACA GTT ATA TGG TAT GAC GGA AGT AAT CAA
P G K G L E W V T V I W Y D G S N Q
TAC TAT ATA GAC TCC GTG AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG
Y Y I D S V K G R F T I S R D N S K
AAC ATG TTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAT ACG GCT GTG TAT
N M L Y L Q M N S L R A E D T A V Y
TAC TGT GCG AGA GAT CGC AAT GGC CTG AAG TAC TTC GAT CTC TGG GGC CGT GGC
Y C A R D R N G L K Y F D L W G R G
D6-19? N padison JH2
ACC CTG GTC ACT GTC TCA TCA GGG AGT GCA TCC GCC CCA ACC CTT TTC CCC CTC
T L V T V S S G S A S A P T L F P L
Cp
GTC TCC TGT GAG AAT TCC CCG TCG GAT ACG AGC 3'
V S C E N S P S D T S

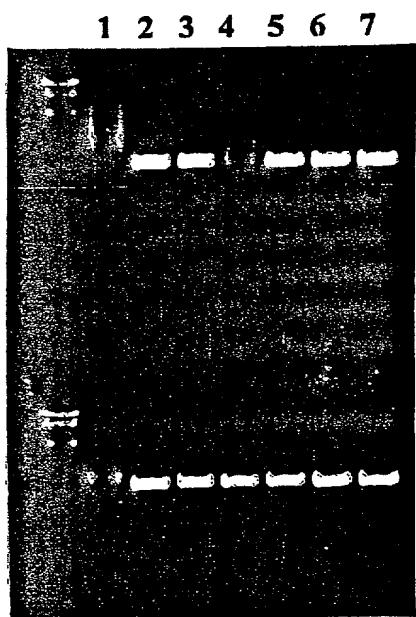
Figure 12B



<u>Fetus</u>	<u>Clone</u>	<u>IgH</u>	<u>Igλ</u>
5580	412	Pos	Pos
5848	214	Neg	Neg

1. Bovine genomic DNA (negative control)
2. Fetus 5580 genomic DNA (Igλ)
3. Fetus 5580 genomic DNA (Igλ)
4. Fetus 5848 genomic DNA (Igλ)
5. Fetus 5848 genomic DNA (Igλ)
6. Positive control (Human genomic DNA)
7. Bovine genomic DNA (negative control)
8. Fetus 5580 genomic DNA (IgH)
9. Fetus 5580 genomic DNA (IgH)
10. Fetus 5848 genomic DNA (IgH)
11. Fetus 5848 genomic DNA (IgH)
12. Positive control (Human genomic DNA)

Figure 13



IgH

1. Bovine genomic DNA (negative control)
2. Fetus 5442A genomic DNA (91 day)
3. Fetus 5442A genomic DNA (91 day)
4. Fetus 5442B genomic DNA (91 day)
5. Fetus 5442B genomic DNA (91 day)
6. Fetus 5968 genomic DNA (56 day; positive control)
7. Human genomic DNA (positive control)

Igλ

Figure 14

1. Bovine spleen (negative control)
2. Fetus 5442A brain
3. Fetus 5442A liver
4. Fetus 5442A spleen
5. Fetus 5442A spleen
6. Fetus 5996 spleen (positive control)
7. Δ HAC-chimeric mouse spleen
(positive control)

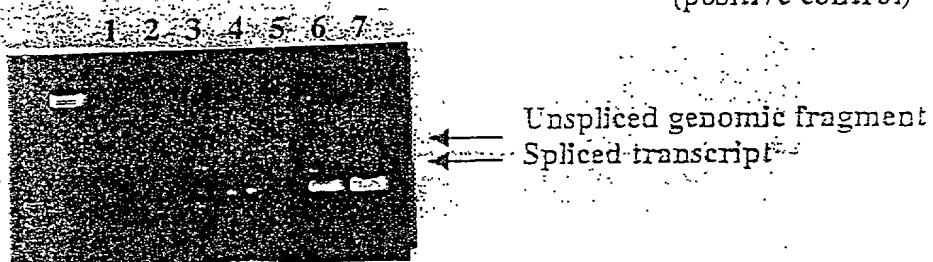
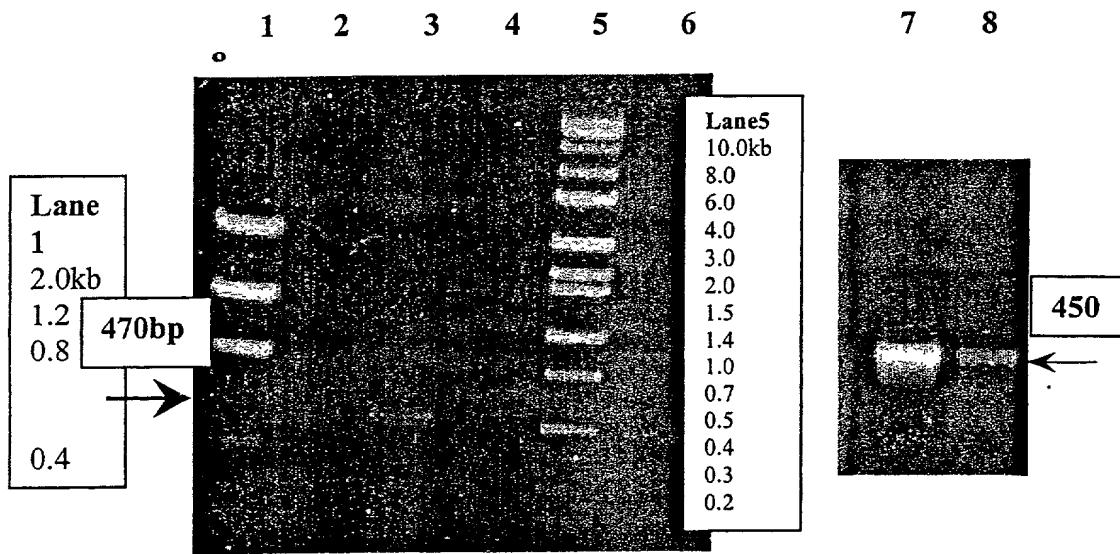


Figure 15



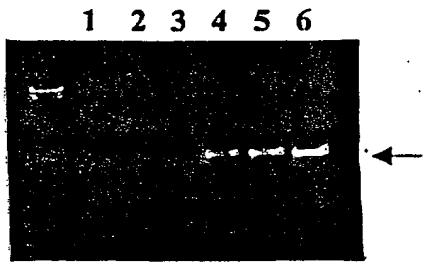
1. Low Mass Ladder: 2.0, 1.2, 0.8, 0.4, 0.2 and 0.1kb
2. Normal Bovine spleen cDNA negative control
3. $\Delta\Delta$ HAC 5868A spleen cDNA
4. empty
5. Hi Lo
:10.0, 6.0, 4.0, 3.0, 2.0, 1.5, 1.4, 1.0, 0.7, 0.5, 0.4, 0.3, 0.2, 0.1kb
6. Tc Mouse HAC spleen cDNA positive control
7. GAPDH product from 5868A spleen cDNA
8. GAPDH product from normal bovine spleen cDNA

Figure 16



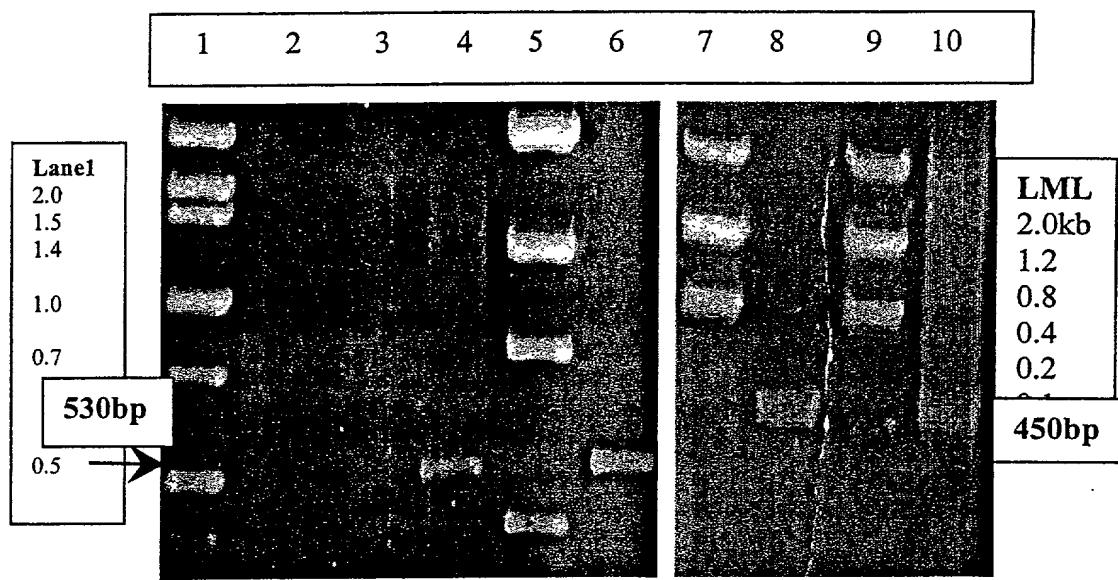
1. Bovine spleen (negative control)
2. Fetus 5442A brain
3. Fetus 5442B brain
4. Fetus 5442A liver
5. Fetus 5442B liver
6. Fetus 5442A spleen
7. Fetus 5442A spleen
8. Fetus 5442B spleen
9. Fetus 5442B spleen
10. Δ HAC-chimeric mouse spleen
(positive control)

Figure 17



1. Bovine spleen (negative control)
2. Fetus 5442A brain
3. Fetus 5442A liver
4. Fetus 5442A spleen
5. Fetus 5442A spleen
6. Δ HAC-chimeric mouse spleen (positive control)

Figure 18



1. Hi-Lo MW:2.0,1.5,1.4,1.0,0.7,0.5 kb
2. $\Delta\Delta$ HAC 5868A fetal brain cDNA
3. $\Delta\Delta$ HAC 5868A fetal liver cDNA
4. $\Delta\Delta$ HAC 5868A fetal spleen cDNA
5. Low Mass Ladder
6. Tc Mouse HAC spleen cDNA positive control (530bp)
7. Low Mass Ladder
8. GAPDH $\Delta\Delta$ HAC 5868A brain cDNA
9. Low Mass Ladder
10. GAPDH $\Delta\Delta$ HAC 5868A liver cDNA

Figure 19

SEG TD Mo₅; 56 and 57

5' ACC CTC CTC ACT CACT TGT GCA GGG TCC TGG GCC CAG TCT GTG ACT CAG CCA
 T L L T H C A G S W A Q S V L T Q P

 CCC TCA CGG TCT GGG ACC CCC GGG CAG AGG GTC ACC ATC TCT TGT TCT GGA AGC
 P S A S G T P G Q R V T I S C S G S

 AGC TCC AAC ATC CGG AGT AAT TAT GTA TAC TGG TAC CAG CAG CTC CCA GGA ACG
 S S N I G S N Y V W Y Q Q L P G T

 GCC CCC AAA CTC CTC ATC TAT AGG AAT AAT CAG CGG CGG CCTCA GGG GTC CCT GAC V 1-17
 A P K L I Y R N N Q R P S G V P D

 CGA TTCT TCT GGCT TCC AAG TCT GGC ACC TCA GCC TCC CTG GCC ATC AGT GGG CTC
 R F S G S K S G T S A S L A I S G L

 CGG TCC GAG GAT GAG GCT GATT TAC TGT GCA GCA TGG GAT GAC AGC CTC AGT
 R S E D E A D Y Y C A A W D D S L S

 GGT CTT TTC GGC GGA GGG ACC AAG CTC ACC GTC CTA GGT CAG CCC AAG GCT GCC
 G L F G G T_{JL3} K L T V L G Q P K A A

 CCC TCG GTC ACT CTG TTC CCA CCC TCC TCT GAG GAG CTT CAA GCC AAC AAG GCC
 P S V T L F P S S E E L Q A N K A

 ACA CTG GTG 3'
 T L V

Figure 20

SEQ ID NO: 58 and 59

5' AGT TGG ACC CCT CTC TGG CTC ACT CTC TTG ACT CTC TTG ATA GGT TCT
S W T P L W L T L F T L C I G S

GTG GTT TCT TCT GAG CTG ACT CAG GAC CCT GCT GTG TCT GTG GCC TGT GGA CG
V V S S E L T Q D P A V S V A L G Q

ACA GTC AGG ATC ACA TGCCAA GGA GAC AGC CTC AGA AGC TAT TAT GCA AGC TGG
T V R I T C Q G D S L R S Y Y A S W

TAC CAG CAG AAG CCA GGA CAG GCC CCT GTACTT GTC ATCTAT GGT AAA AAC AAC V2-13
Y Q K P G Q A P V L V I Y G K N N

CGG CCC TCA GGG ATCCA GAC CGA TTCTCT GGCTCC AGCTCA GGA AAC ACA GCT
R P S G I P D R F S G S S G N T A

TCC TTG ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG GCT GACT ATT TAC TGT AAC
S L T I T G A Q A E D E A D Y Y C N

TCC CGG GAC AGC AGT GGT AAC CAT CTG GTA TTC GGC GGA GGG ACC AAG CTG ACC JL2
S R D S S G N H L V F G G T K L T

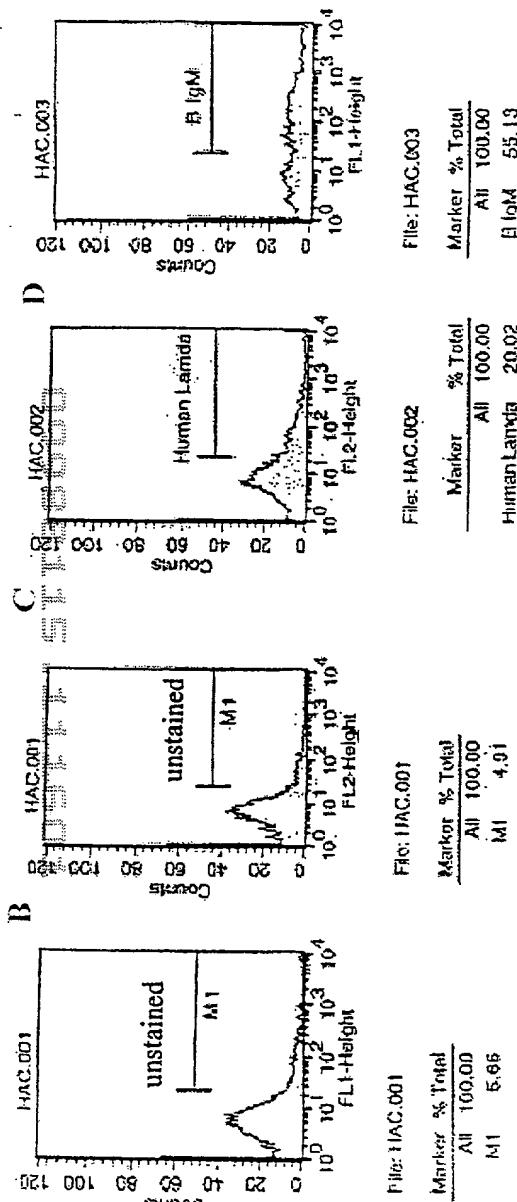
GTC CTA GGT CAG CCC AAG GCT GCC CCC TCG ACT CTG TTG CCA CCC TCC TCT
V L G Q P K A A P S V T L F P S S

GAG GAG CTT CAA GCC AAC AAG GCC ACA CTG GTG 3'
E E L Q A N K A T L V
CA

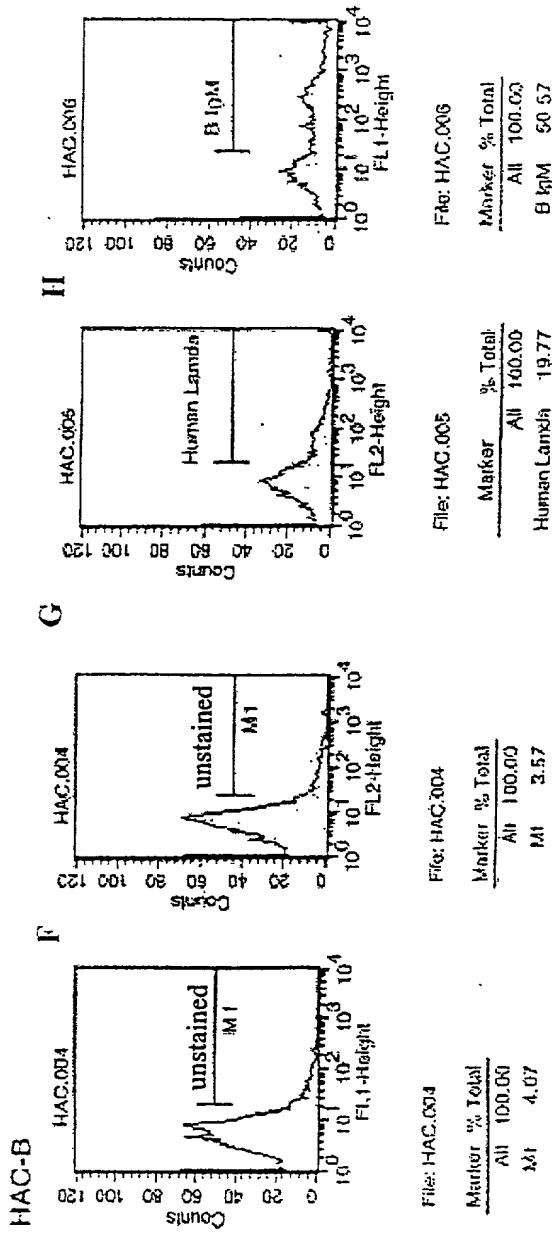
Figure 21

Figure 22A - 22H

Fetus #5442A



Fetus #5442B



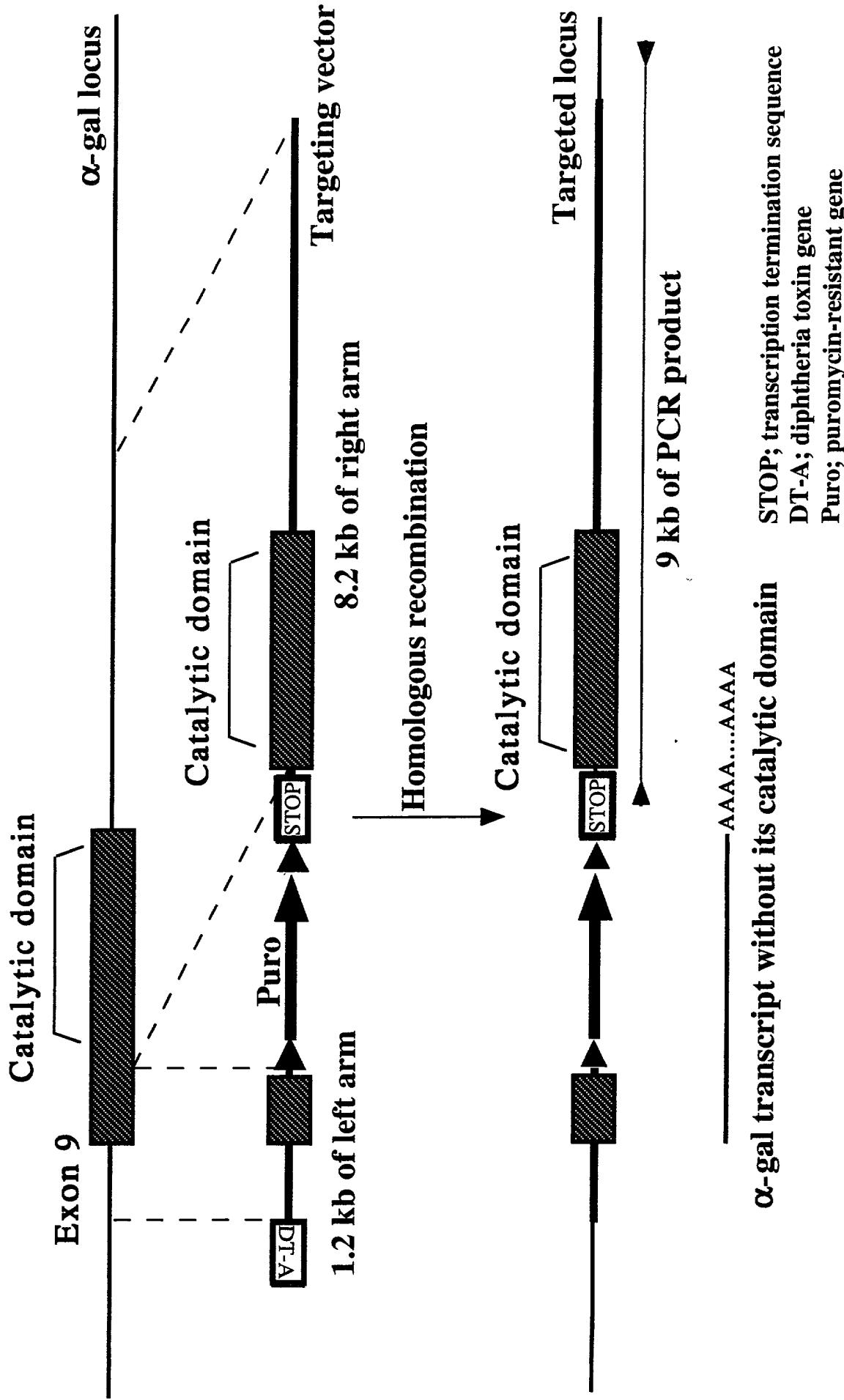
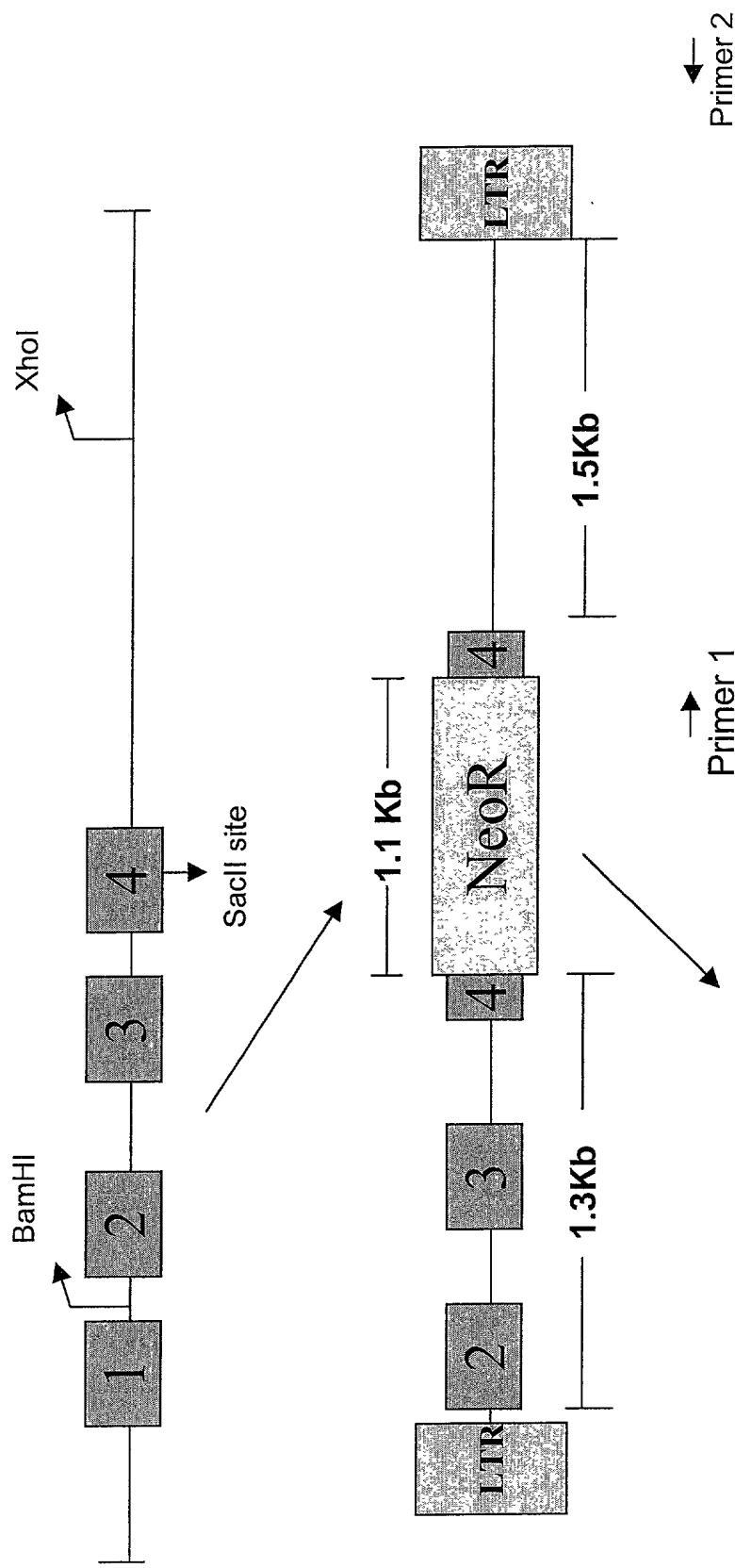


Figure 23



PACKAGE AAV PARTICLES

Figure 24

Figure 25

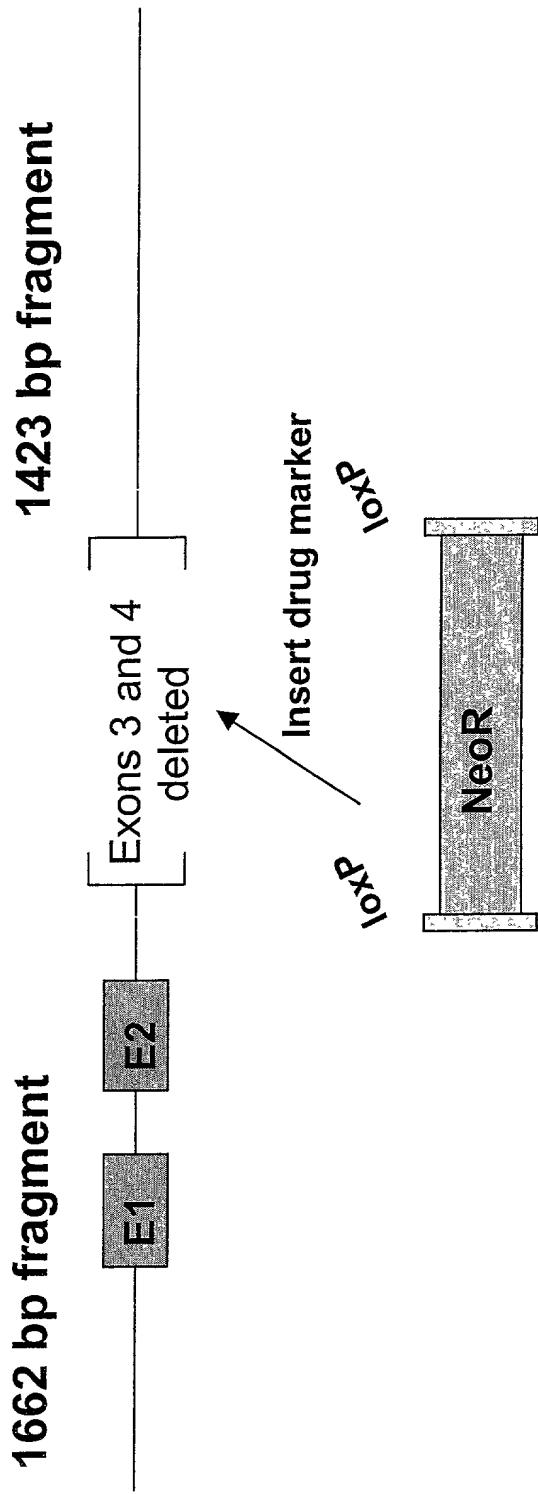


Figure 26

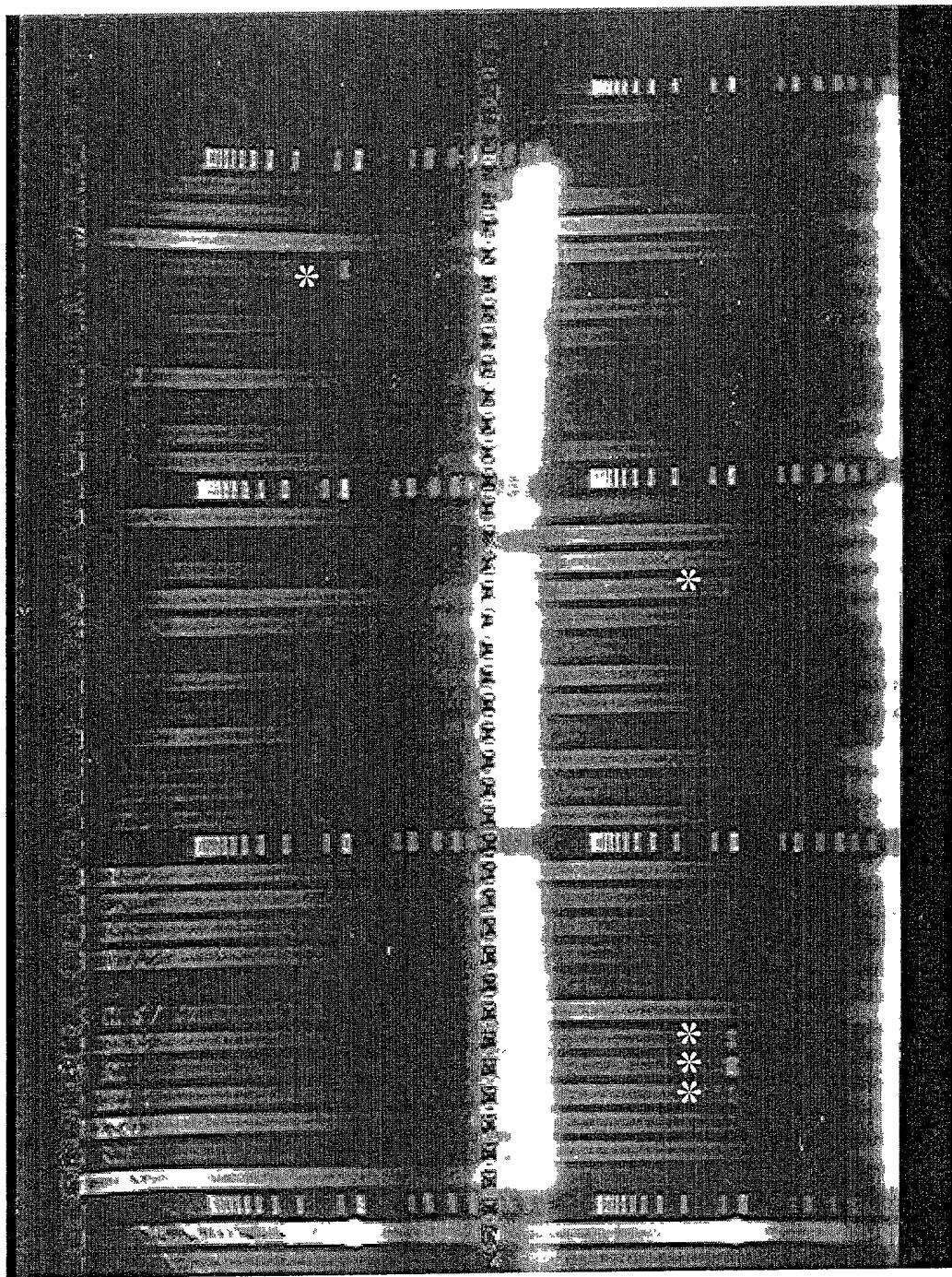


Figure 27

NT, ET and pregnancies :Delta HAC regenerated fibroblasts									
Cell line	ID	Total NT's in culture	No of Blast (%)	No of Blast Transferred	No Recinos	Pregnancy status			
						40 d	60 d	90 d	120 d
D5668	174	34 (28)	27	17	3	3	3	3	3
D6045	215	10 (7)	8	4	1	1	1	1	1
D6045	122	20 (23)	12	9	1	0	0	0	0
D6032	161	18 (16)	14	7	3	3	3	2	2
D6032	183	15 (11)	11	11	3	0	0	0	0
D6032	198	20 (14)	16	10	1	1	1	1	1
D6032	200	17 (12)	12	8	2	2	2	2	2
D6032	180	11 (9)	10	5	3	1	1	1	0
D6032	135	22 (23)	22	11	2	1	1	1	1
D5668	140	35 (36)	25	13	2	2	2	2	1
D5668	180	30 (24)	26	13	2	2	2	2	1
D6045	170	46 (39)	32	16	4				
D6045	80	7 (13)	1	1	0				
D6045 SLOT	108	9 (12)	3	2	1				
D6045	76	8 (15)	2	1	0				
D6045 SLOT	128	12 (13)	7	5	0				
D6045	47	6 (18)	5	3	3				
D6045 SLOT	112	3 (4)	3	2	2				
D6045	120	28 (33)	18	9					
D6045 SLOT	100	11 (16)	2	1					
D6045	78	15 (27)	16	8					
D6045 SLOT	91	0	2	1					
D6045	98	16 (23)	10	5					
D6045 SLOT	104	16 (22)	10	5					
D5668	128	24 (27)	8	4					
D5668 SLOT	65	10 (22)	8	4					
D5668	120	28 (33)	14	7					
D5668 SLOT	95	13 (19)	6	3					
D5668	98	17 (25)	10	6					
D5668 SLOT	93	14 (22)	12	6					
D	13	1 (11)	1	3					
SLOT	63	8 (18)	8	3					
D	4	(5)	4	3					
SLOT	100	1 (1)	1	3					
D	90	10 (16)	10	6					
SLOT	110	13 (17)	13	6					
D	90	10 (16)	10	1					
SLOT	83	5 (9)	5	1					
D	105	20 (27)	20	9					
SLOT	78	7 (13)	7	2					
D	88	7 (11)	7	4					
SLOT	93	9 (14)	9	4					
D	85	20 (33)	20	10					
SLOT	77	4 (7)	4	2					
	4987	515 (19)	481	258					
Summary		No of Pregnancies							
Preg Status		> 40 d	9						
		> 90 d	2						
		> 120 d	4						
		> 180 d	3						
		> 210 d	3						
Total			21						